

GenCore version 5.1.7  
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OW protein - protein search, using sw model

Run on: May 5, 2006, 13:58:01 ; Search time 46 Seconds  
(without alignments)  
564.351 Million cell updates/sec

Title: US-10-666-851-2

Sequence: 1 MGIRSEGGRRGALGVLLA.....KFMKMKMKHCEPTQSVFK 314

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5 COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/6 COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/8 COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/PCPUS\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/RE\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1701	99.7	314	2	US-08-937-067-7	Sequence 7, Appl1
2	1691.5	99.2	313	2	US-09-514-885-1	Sequence 1, Appl1
3	1691.5	99.2	313	2	US-09-949-016-6239	Sequence 6299, Ap
4	1657.5	97.2	313	2	US-09-546-043-3	Sequence 3, Appl1
5	1657.5	97.2	313	2	US-09-546-043-4	Sequence 4, Appl1
6	1629	95.5	314	2	US-09-087-031B-3	Sequence 3, Appl1
7	1614.5	94.6	313	2	US-09-087-031B-4	Sequence 4, Appl1
8	1267.5	74.3	267	2	US-09-546-043-6	Sequence 7, Appl1
9	1171	68.6	246	2	US-09-546-043-6	Sequence 6, Appl1
10	971	56.9	229	2	US-09-546-043-8	Sequence 8, Appl1
11	924.5	54.2	317	2	US-08-937-067-6	Sequence 6, Appl1
12	924.5	54.2	317	2	US-09-949-016-6300	Sequence 6300, Ap
13	911.5	53.4	317	2	US-09-949-016-7706	Sequence 7706, Ap
14	887.5	52.0	195	2	US-09-546-043-5	Sequence 5, Appl1
15	605.5	35.5	295	2	US-08-937-067-2	Sequence 2, Appl1
16	598	35.1	295	2	US-09-999-833A-415	Sequence 415, App
17	598	35.1	295	2	US-10-020-445A-415	Sequence 415, App
18	597	35.0	295	2	US-09-148-545-179	Sequence 179, App
19	597	35.0	295	2	US-09-621-011-179	Sequence 179, App
20	597	35.0	296	2	US-09-148-545-237	Sequence 237, App
21	597	35.0	296	2	US-09-621-011-237	Sequence 237, App
22	594	34.8	109	2	US-09-087-031B-19	Sequence 19, Appl1
23	508.5	29.8	295	2	US-08-893-654B-6	Sequence 6, Appl1
24	436	25.6	212	2	US-08-937-067-4	Sequence 4, Appl1
25	409.5	24.0	280	2	US-08-893-654B-4	Sequence 4, Appl1
26	387	22.7	281	2	US-08-893-654B-2	Sequence 2, Appl1
27	353	20.7	113	2	US-09-087-031B-24	Sequence 24, Appl1

28	272.5	16.0	572	2	US-08-937-067-13	Sequence 13, Appl1
29	262.5	15.4	537	2	US-08-937-067-11	Sequence 11, Appl1
30	262	15.4	319	2	US-10-014-055-7	Sequence 7, Appl1
31	258	15.1	319	2	US-10-014-055-8	Sequence 8, Appl1
32	258	15.1	319	2	US-10-028-051A-7	Sequence 7, Appl1
33	258	15.1	565	2	US-08-937-067-8	Sequence 8, Appl1
34	253.5	14.9	325	2	US-10-014-055-2	Sequence 2, Appl1
35	253.5	14.9	325	2	US-10-028-051A-2	Sequence 2, Appl1
36	252	14.8	318	2	US-08-878-474-3	Sequence 3, Appl1
37	248	14.5	319	2	US-10-028-051A-8	Sequence 8, Appl1
38	247.5	14.5	323	2	US-08-878-474-7	Sequence 7, Appl1
39	247.5	14.5	325	2	US-08-878-474-9	Sequence 9, Appl1
40	247.5	14.5	325	2	US-09-976-594-479	Sequence 479, App
41	247.5	14.5	325	2	US-10-014-055-4	Sequence 4, Appl1
42	247.5	14.5	325	2	US-10-028-051A-4	Sequence 4, Appl1
43	247.5	14.5	371	2	US-09-949-016-7544	Sequence 7544, Ap
44	244	14.3	111	2	US-10-014-055-5	Sequence 5, Appl1
45	244	14.3	111	2	US-10-028-051A-5	Sequence 5, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-937-067-7  
Sequence 7, Application US/08937067  
Patent No. 643355

GENERAL INFORMATION:

APPLICANT: Umanaky, Samu1

TITLE OF INVENTION: A FAMILY OF GENES ENCODING

TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND

TITLE OF INVENTION: METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:

ADDRESSER: MORRISON & FORSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,067

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 314 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-937-067-7

Query Match 99.7%; Score 1701; DB 2; Length 314;  
Best Local Similarity 99.7%; Pred. No. 3.5e-174;  
Matches 313; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGIRSEGGRRGALGVLLAALAVGASRYDVVSFSDIGFPGVGRFYYKPPQCVN 60  
DB 1 MGIRSEGGRRGALGVLLAALAVGASRYDVVSFSDIGFPGVGRFYYKPPQCVN 60

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QY 61 IPADRLCHNVGYKKMVLNLLHETMAVKKOASWVPLLNKNGCHAGTVFLCSLFAV 120
DB 61 IPADRLCHNVGYKKMVLNLLHETMAVKKOASWVPLLNKNGCHAGTVFLCSLFAV 120
QY 121 CLDRPIYPCRMUCEAVRDSCEPVMOFGFYWPEMLKCDKFPBGDVCIAINTPPNATEASRP 180
DB 121 CLDRPIYPCRMUCEAVRDSCEPVMOFGFYWPEMLKCDKFPBGDVCIAINTPPNATEASRP 180
QY 181 OGTTVCPCDNLKSEBAILIEHLCASEFALRMKIKVKKENGDKKIVPKKKKPLKGLPIK 240
DB 181 OGTTVCPCDNLKSEBAILIEHLCASEFALRMKIKVKKENGDKKIVPKKKKPLKGLPIK 240
QY 241 KDLKLVLYLKNAGADCPCHQDNLNLSHFLIMGRKVSQYLLTAIHKMDKKNKBFKPMK 300
DB 241 KDLKLVLYLKNAGADCPCHQDNLNLSHFLIMGRKVSQYLLTAIHKMDKKNKBFKPMK 300
QY 301 MKNHECPTFQSVFK 314
DB 301 MKNHECPTFQSVFK 314

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## RESULT 2

```

US-09-514-885-1
; Sequence 1, Application US/09514885
; Patent No. 6656461
; GENERAL INFORMATION:
; APPLICANT: D'Armenteo, Jeanine
; APPLICANT: Imai, Kazuhi
; TITLE OF INVENTION: NOVEL THERAPEUTIC TREATMENT OF CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 58483.add
; CURRENT APPLICATION NUMBER: US/09/514, 885
; CURRENT FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Human
US-09-514-885-1

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Query Match 99.2%; Score 1691.5; DB 2; Length 313;
Best Local Similarity 99.7%; Pred. No. 3.6e-173;
Matches 313; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 1 MGIGRSEGGRRGALGVLLALGALLAVGSASEYDVSPQSDIGPYQSGRFTTKPQCVD 60
DB 1 MGIGRSEGGRRG-ALGVLLALGALLAVGSASEYDVSPQSDIGPYQSGRFTTKPQCVD 59
QY 61 IPADRLCHNVGYKKMVLNLLHETMAVKKOASWVPLLNKNGCHAGTVFLCSLFAV 120
DB 61 IPADRLCHNVGYKKMVLNLLHETMAVKKOASWVPLLNKNGCHAGTVFLCSLFAV 119
QY 121 CLDRPIYPCRMUCEAVRDSCEPVMOFGFYWPEMLKCDKFPBGDVCIAINTPPNATEASRP 180
DB 121 CLDRPIYPCRMUCEAVRDSCEPVMOFGFYWPEMLKCDKFPBGDVCIAINTPPNATEASRP 179
QY 181 OGTTVCPCDNLKSEBAILIEHLCASEFALRMKIKVKKENGDKKIVPKKKKPLKGLPIK 240
DB 181 OGTTVCPCDNLKSEBAILIEHLCASEFALRMKIKVKKENGDKKIVPKKKKPLKGLPIK 239
QY 241 KDLKLVLYLKNAGADCPCHQDNLNLSHFLIMGRKVSQYLLTAIHKMDKKNKBFKPMK 300
DB 241 KDLKLVLYLKNAGADCPCHQDNLNLSHFLIMGRKVSQYLLTAIHKMDKKNKBFKPMK 299
QY 301 MKNHECPTFQSVFK 314
DB 301 MKNHECPTFQSVFK 313

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```

RESULT 3
US-09-949-016-6299
; Sequence 6299, Application US/09949016

```

```

; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6299
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6299

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Query Match 99.2%; Score 1691.5; DB 2; Length 313;
Best Local Similarity 99.7%; Pred. No. 3.6e-173;
Matches 313; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 1 MGIGRSEGGRRGALGVLLALGALLAVGSASEYDVSPQSDIGPYQSGRFTTKPQCVD 60
DB 1 MGIGRSEGGRRG-ALGVLLALGALLAVGSASEYDVSPQSDIGPYQSGRFTTKPQCVD 59
QY 61 IPADRLCHNVGYKKMVLNLLHETMAVKKOASWVPLLNKNGCHAGTVFLCSLFAV 120
DB 61 IPADRLCHNVGYKKMVLNLLHETMAVKKOASWVPLLNKNGCHAGTVFLCSLFAV 119
QY 121 CLDRPIYPCRMUCEAVRDSCEPVMOFGFYWPEMLKCDKFPBGDVCIAINTPPNATEASRP 180
DB 121 CLDRPIYPCRMUCEAVRDSCEPVMOFGFYWPEMLKCDKFPBGDVCIAINTPPNATEASRP 179
QY 181 OGTTVCPCDNLKSEBAILIEHLCASEFALRMKIKVKKENGDKKIVPKKKKPLKGLPIK 240
DB 181 OGTTVCPCDNLKSEBAILIEHLCASEFALRMKIKVKKENGDKKIVPKKKKPLKGLPIK 239
QY 241 KDLKLVLYLKNAGADCPCHQDNLNLSHFLIMGRKVSQYLLTAIHKMDKKNKBFKPMK 300
DB 241 KDLKLVLYLKNAGADCPCHQDNLNLSHFLIMGRKVSQYLLTAIHKMDKKNKBFKPMK 299
QY 301 MKNHECPTFQSVFK 314
DB 301 MKNHECPTFQSVFK 313

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RESULT 4
US-09-546-043-3
; Sequence 3, Application US/09546043
; Patent No. 6600018
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffrey et al.
; TITLE OF INVENTION: SECRETED FRITZLED RELATED PROTEIN, sFRP, FRAGMENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 53990
; CURRENT APPLICATION NUMBER: US/09/546,043
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-546-043-3

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Query Match 97.2%; Score 1657.5; DB 2; Length 313;
Best Local Similarity 97.5%; Pred. No. 1.6e-169;
Matches 306; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

```

XX New secreted frizzled-related protein-1-binding peptide, for enhancing or  
PT stimulating osteoclast differentiation or to modify T-cell activity in a  
PT subject with e.g. abnormal bone remodeling, achondroplasia or  
PT osteopetrosis.  
XX  
XX Example, Page 74-75; 81pp; English.  
XX  
CC The invention relates to a purified peptide that binds to secreted  
CC frizzled-related protein (sFRP)-1. The peptide is useful for enhancing or  
CC stimulating osteoclast differentiation, or to modify T-cell activity in a  
CC subject with abnormal bone remodeling, achondroplasia, Albright's  
CC osteodystrophy or osteopetrosis. The sFRP-1 is useful for inhibiting  
CC osteoclast formation in a subject with a bone disorder or unwanted bone  
CC resorption, e.g. postmenopausal osteoporosis, Paget's disease, lytic bone  
CC metastases, multiple myeloma, rheumatoid arthritis or hypercalcemia of  
CC malignancy. Modulating T-cell activity is useful in subjects suspected of  
CC having toxic shock, sepsis, graft-versus-host reactions or acute  
CC inflammatory reactions. The immunostimulatory sFRP-1-binding peptide is  
CC useful in activating the immune system against bacterial, viral and  
CC parasitic infections, and in the treatment of human immunodeficiency  
CC virus (HIV). The present sequence represents a human sFRP-1 netrin  
CC homology domain  
CC  
CC Sequence 141 AA;  
SQ  
XX  
XX Query Match 100.0%; Score 78; DB 5; Length 141;  
XX Best Local Similarity 100.0%; Pred. No. 0.00046;  
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 KKEGDKKIVPKKK 15  
DB 52 KKEGDKKIVPKKK 66  
XX  
XX RESULT 2  
XX ID AAY48493 standard; protein; 148 AA.  
XX AAY48493;  
XX  
XX AAY48493;  
XX  
XX 08-DEC-1999 (first entry)  
XX  
XX Human breast tumour-associated protein 38.  
XX  
XX Expressed sequence tag; EST; human; breast; cancer; cytostatic;  
XX medicaments; gene therapy; treatment; fat metabolism.  
XX  
XX Homo sapiens.  
XX  
XX DE19813835-A1.  
XX  
XX 23-SEP-1999.  
XX  
XX 20-MAR-1998; 98DE-01013835.  
XX  
XX 20-MAR-1998; 98DE-01013835.  
XX  
XX (METRA-) METRAGEN GES GENOMFORSCHUNG MBH.  
XX  
XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;  
XX WPI; 1999-528979/45.  
XX  
XX N-PSDB; AAZ33577.  
XX  
XX Human nucleic acid sequences and protein products from normal breast  
XX tissue, useful for breast cancer therapy.  
XX  
XX Claim 26; 175; 206pp; German.  
XX  
XX This invention describes novel human nucleic acid sequences from normal  
XX breast tissue which have cytostatic activity. The nucleic acid sequences  
XX can be used to produce and isolate full-length gene sequences. They can

CC be used to express proteins, which can be used as tools to find an  
CC activity against breast cancer. The sequences can be used in sense or  
CC antisense form. They are especially useful for medicaments for gene  
CC therapy to treat breast cancer and for treating illnesses associated with  
CC fat metabolism. AAY48456-Y48539 represent protein fragments encoded by  
CC the expressed sequence tags described in the method of the invention  
XX  
XX Sequence 148 AA;  
SQ  
XX  
XX Query Match 100.0%; Score 78; DB 2; Length 148;  
XX Best Local Similarity 100.0%; Pred. No. 0.00048;  
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 KKEGDKKIVPKKK 15  
DB 51 KKEGDKKIVPKKK 65  
XX  
XX RESULT 3  
XX ID ADR09139 standard; protein; 178 AA.  
XX ADR09139;  
XX  
XX ADR09139;  
XX  
XX 04-NOV-2004 (first entry)  
XX  
XX  
XX Human protein useful for treating neurological disease Seq 2645.  
XX  
XX human; oligo-capping method; diagnostic marker; gene therapy;  
XX osteoporosis; neurological disease; Alzheimer's disease;  
XX Parkinson's disease; dementia; short memory; cancer;  
XX sense or motor function; emotional reaction; fear response; panic;  
XX osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;  
XX tranquilliser.  
XX  
XX Homo sapiens.  
XX  
XX EP1447413-A2.  
XX  
XX 18-AUG-2004.  
XX  
XX 12-FEB-2004; 2004EP-00003145.  
XX  
XX 14-FEB-2003; 2003JP-00102207.  
XX  
XX 09-MAY-2003; 2003JP-00131452.  
XX  
XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;  
XX Wakamatsu A, Ishii S, Nagai K, Irie R;  
XX WPI; 2004-583265/57.  
XX  
XX N-PSDB; ADR07183.  
XX  
XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,  
XX Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.  
XX  
XX Claim 1; SEQ ID NO 2645; 2686pp; English.  
XX  
XX This invention relates to novel, isolated full length human cDNA  
XX molecules and the encoded proteins thereof. Specifically, it refers to  
XX cDNA clones obtained by an oligo-capping method, where none of these  
XX clones are identical to any known human mRNA. The present invention  
XX describes an immunosay to identify agonists and antagonists, as well as  
XX antibodies, antisense molecules and siRNAs that can all be used to bind  
XX to and modulate expression of the cDNA molecules. As such, these  
XX molecules are useful for diagnostic markers or therapeutic targets for  
XX the various diseases or morbid states. In particular, they are useful in  
XX gene therapy for treating osteoporosis, neurological disease, Alzheimer's  
XX disease, Parkinson's disease, dementia, short memory and various cancers,  
XX as well as for maintaining equilibrium of sense or motor function, and  
XX for treating emotional reaction, fear response and panic. Accordingly,  
XX they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: May 5, 2006, 13:50:51 ; Search time 229 Seconds  
(without alignments)  
967.406 Million cell updates/sec

Title: US-10-666-851-2  
Perfect score: 1706  
Sequence: 1 MGIGRSGRGGRAALGVTLA.....KNFMKMKMKHNCPTFQSVFK 314

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: 1: uniprot\_05.80.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	1706	100.0	314	1 SFRP1_HUMAN	O8N474 homo sapien
2	1626	95.3	314	2 O505A2_MOUSE	O505A2 mus musculu
3	1623	95.1	314	1 SFRP1_MOUSE	O8C4U3 mus musculu
4	1607	94.2	308	1 SFRP1_BOVIN	O19116 bos taurus
5	1489	87.3	314	1 SFRP1_CHICK	O9D6Q4 gallus galli
6	1100.5	64.5	306	2 O6GZK1_ORYLA	O6GZK1 oryzias lat
7	1092.5	64.0	321	2 O4SKX3_TETNG	O4SKX3 tetradodon n
8	1084	63.5	311	2 O9Y124_XENLA	O9Y124 xenopus lae
9	1070.5	62.7	310	2 O6YNR8_BRARE	O6YNR8 brachydantio
10	1012	59.3	296	2 O4RGR2_BRARE	O4RGR2 brachydantio
11	955.5	56.0	311	2 O4RGR2_TETNG	O4RGR2 tetradodon n
12	947.5	55.5	281	2 O568X0_BRARE	O568X0 brachydantio
13	946	55.5	315	2 O6G450_XENLA	O6G450 xenopus tro
14	945	55.4	315	2 O640J3_XENLA	O640J3 xenopus lae
15	942.5	55.2	315	2 O6AWG4_XENLA	O6AWG4 xenopus lae
16	924.5	54.2	314	1 SFRP1_HUMAN	O6T447 homo sapien
17	922.5	54.1	314	1 SFRP5_MOUSE	O6W466 mus musculu
18	916.5	53.7	315	1 SFRP5_BOVIN	O6X6C1 bos taurus
19	844	49.5	158	1 SFRP1_PAT	O9R168 rattus norv
20	718	42.1	178	2 O6ZS14_HUMAN	O6ZS14 homo sapien
21	658.5	38.6	295	2 O6P8B8_XENLA	O6P8B8 xenopus tro
22	649	38.0	295	2 O4SS00_TETNG	O4SS00 tetradodon n
23	645.5	37.8	298	2 O7ZXM6_XENLA	O7ZXM6 xenopus lae
24	629	36.9	282	2 O8JHC7_BRARE	O8JHC7 brachydantio
25	610	35.8	294	1 SFRP2_CANFA	O86JH1 canis famli
26	610	35.8	365	2 O4H2U5_CIOIN	O4H2U5 ctiona inres
27	605.5	35.5	292	1 SFRP2_CHICK	O6I8A6 gallus galli
28	605.5	35.5	295	1 SFRP2_MOUSE	P97299 mus musculu
29	602	35.3	293	1 SFRP2_HUMAN	O96H11 homo sapien
30	595.5	34.9	283	2 O9BGS6_PABIT	O9BGS6 oryctolagus
31	541.5	31.7	307	2 O42397_CHICK	O42397 gallus galli

32	515	30.2	300	2 O6F2E8_XENLA	O6F2E8 xenopus tro
33	508.5	29.8	295	2 O91897_XENLA	O91897 xenopus lae
34	463	27.1	293	2 O4H2U4_CIOIN	O4H2U4 ctiona inres
35	433	25.4	115	2 O90ZG8_BRARE	O90ZG8 brachydantio
36	413	24.2	281	2 O73821_XENLA	O73821 xenopus lae
37	412	24.2	130	2 O52K37_CHICK	O52K37 gallus galli
38	409.5	24.0	280	2 O9IAU5_XENLA	O9IAU5 xenopus lae
39	395	23.2	282	2 O4RS17_TETNG	O4RS17 tetradodon n
40	392.5	23.0	284	2 O90ZAG_AMBER	O90ZAG ambystoma m
41	390.5	22.9	261	2 O61U61_CAER	O61U61 caenorhabdi
42	385	22.6	260	2 O9GUP5_CAERL	O9GUP5 caenorhabdi
43	369.5	21.7	282	2 O7SX78_BRARE	O7SX78 brachydantio
44	369.5	21.7	289	2 O504J9_BRARE	O504J9 brachydantio
45	295	17.3	592	1 FZD1_CHICK	O57328 gallus galli

#### ALIGNMENTS

RESULT 1  
SFRP1\_HUMAN STANDARD; PRT; 314 AA.  
ID SFRP1\_HUMAN  
AC O8N474; 000546; O14779;  
DT 10-MAY-2005 (Rel. 47, Created)  
DT 10-MAY-2005 (Rel. 47, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Secreted Frlizled-related protein 1 precursor (SFRP-1) (Frlizled-related protein 1) (FRP-1) (Secreted apoptosis-related protein 2) (SARP-2).  
GN Name=SFRP1; Synonyms=FRP, FRP1, SARP2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA], AND PROTEIN SEQUENCE OF 39-78.  
RC TISSUE=Embryonic lung fibroblast;  
RX MEDLINE=97338093; PubMed=9192640; DOI=10.1073/pnas.94.13.6770;  
RA Finch P.W., He X., Kelley M.J., Uren A., Schaudies R.P., Popescu N.C., Rudnikoff S., Aaronson S.A., Varmus H.E., Rubin J.S.;  
RT "Purification and molecular cloning of a secreted, Frlizled-related antagonist of Wnt action.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:6770-6775(1997).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [MRNA], AND TISSUE SPECIFICITY.  
RC TISSUE=Heart;  
RX MEDLINE=98054286; PubMed=9391078; DOI=10.1073/pnas.94.25.13636;  
RA Melkonian H.S., Chang W.C., Shapiro J.P., Mahadevappa M., Fitzpatrick P.A., Klefer M.C., Tomei L.D., Umaneky S.R.;  
RT "SARpe: a family of secreted apoptosis-related proteins.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:13636-13641(1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [MRNA], AND INDUCTION.  
RX PubMed=9724099;  
RA Zhou Z., Wang J., Han X., Zhou J., Linder S.;  
RT "Up-regulation of human secreted Frlizled homolog in apoptosis and its down-regulation in breast tumors.";  
RL Int. J. Cancer 78:95-99(1998).  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg K.H., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusika K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Pringle C., Bork S.S., Iqbaliano N.A., Peters G.J., Abramson R.D., Mullaney S.J., Rana S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,

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OM protein - protein search, using sw model

Run on: May 5, 2006, 13:54:06 / Search time 39 Seconds  
(without alignments)  
774.668 Million cell updates/sec

Title: US-10-666-851-2

Perfect score: 1706

Sequence: 1 MGIGRSGRGRGALGVLLA.....KNFMKKMKHCEPTFQSVF 314  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	917.5	53.8	317	JB0175	freezed protein-1
2	602	35.3	295	JB0174	freezed protein-2
3	276.5	16.2	574	JB0339	freezed-7 protein
4	273.5	16.0	568	T25162	freezed-1 protein
5	271.5	15.9	537	JC7127	freezed protein 4
6	265	15.5	647	JB0337	freezed-1 protein
7	264	15.5	581	S03540	gene freezed prot
8	258	15.1	565	JB0338	freezed-2 protein
9	256.5	15.0	581	JC7086	freezed-2 protein
10	252.5	14.8	641	A45054	freezed-2 protein
11	237.5	13.9	550	T37325	freezed-2 protein
12	228.5	13.4	694	S71786	freezed-2 protein
13	223.5	13.1	197	JC7735	freezed-2 protein
14	215	12.6	666	JB0332	freezed-2 protein
15	215	12.6	706	JB0164	freezed-2 protein
16	201	11.8	605	T31690	freezed-2 protein
17	201	11.8	1113	JB0315	freezed-2 protein
18	170.5	10.0	1774	B56101	freezed-2 protein
19	133.5	7.8	526	T13484	freezed-2 protein
20	132.5	7.8	579	JB0629	freezed-2 protein
21	125	7.3	793	JB0539	freezed-2 protein
22	107.5	6.3	549	B86337	freezed-2 protein
23	97	5.7	785	S46672	freezed-2 protein
24	97	5.7	2228	T14029	freezed-2 protein
25	96.5	5.7	1024	S71804	freezed-2 protein
26	96.5	5.7	1150	T15277	freezed-2 protein
27	93.5	5.5	1474	D88550	freezed-2 protein
28	93	5.5	527	SAHUP	freezed-2 protein
29	92.5	5.4	1051	JC4091	freezed-2 protein

30	91	5.3	260	T01837	hypothetical prote
31	91	5.3	527	A42032	epidermal growth f
32	91	5.3	1008	C84679	hypothetical prote
33	91	5.3	1077	T21800	hypothetical prote
34	91	5.3	1223	1 TVCHLV	epidermal growth f
35	90.5	5.3	1751	T09394	gag-pro-pol polypr
36	89.5	5.2	792	A70476	ATP-dependent DNA
37	88	5.2	718	T51488	hypothetical prote
38	88	5.2	1051	S55259	TIF1 protein - mou
39	87.5	5.1	1097	A56138	transcription fact
40	87.5	5.1	4152	T31102	filamentous hemagg
41	87.5	5.1	4919	T31105	hypothetical prote
42	87	5.1	578	C64452	restriction modifi
43	87	5.1	1699	T14074	complement compone
44	86.5	5.1	623	A49112	sodium-glucose cot
45	86.5	5.1	1001	S30385	G9a protein - huma

## ALIGNMENTS

RESULT 1  
JB0175  
freezed protein-1b - human  
C/Species: Homo sapiens (man)  
C/Date: 03-Jul-1998 #sequence\_revision 10-Jul-1998 #text\_change 09-Jul-2004  
C/Accession: JB0175  
R:Hu, B.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.  
Biochem. Biophys. Res. Commun. 247, 287-293, 1998  
A/Title: Tissue restricted expression of two human fibro in preadipocytes and pancreas.  
A/Reference number: JB0174; WUID:98308108; PMID:9642118  
A/Accession: JB0175  
A/Molecule type: mRNA  
A/Residues: 1-317 <HUA>  
A/Cross-references: UNIPROT:O14780; UNIPARC:UP10000158811  
C/Genetics:  
A/Gene: hPRP-1b  
A/Map position: 5q14.3-q12.1

Query Match 53.8%; Score 917.5; DB 2; Length 317;  
Best Local Similarity 56.3%; Pred. No. 56-69;  
Matches 178; Conservative 51; Mismatches 78; Indels 9; Gaps 6;

QY	1	MGIGRSGRGRGALGVLLA	GAALAVGSASEDYVSPQSDIGPYGGRPYTKPQCV	60
DB	1	MRBAAAAGVTRTAAALL	LGALHMAPACBETHYGMQAB--PLH-GRSYSGPQC	55
QY	61	IPADLRCANVGYKQVLP	MLHETMAEYKQASVPLANKCAGTGFCSLP	120
DB	56	IPADLPCHTVGYKRMRL	PLHREHSLAEVYKQASVPLAARCHSDTVFCSLP	115
QY	121	CLBRPIYPCRMWLC	CAVADSCPEVMPFGFVPMKCDKRP-BGDVCIANTP	179
DB	116	CLBRPIYPCRMWLC	CAVADSCPEVMPFGFVPMKCDKRP-BGDVCIANTP	174
QY	180	PGSTVCPPCDNEIK	SBATIEHLCAISFALRMKIKVKKENSGDKTV--PKKKPL	237
DB	175	PVPTKICACQEMESH	ADGLMEQCSSDFVYKMKIKIKINGRKILGAOKKKL	234
QY	238	IKKKDLKLVLY	LKNGADCECHLDNLSHFPLMGRVYSQYLLTAHKKDK	297
DB	235	LKKRDKTRLV	LHNMKNAGCPCQLDLSLAGFLVMGRKVDQLLIMAYR	294
QY	298	MKGKMKHCEPTFQSV	F 313	
DB	295	VKMFSTPCSLTYPP	F 310	

RESULT 2  
JB0174  
freezed protein-2 - human  
C/Species: Homo sapiens (man)  
C/Date: 03-Jul-1998 #sequence\_revision 10-Jul-1998 #text\_change 09-Jul-2004

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OM protein - protein search, using sw model

Run on: May 5, 2006, 13:50:11 ; Search time 186 Seconds  
(without alignments)  
741.747 Million cell updates/sec

Title: US-10-666-851-2

Sequence: 1706  
1 MGIHSEGRGALGVLLA.....KNFMKKMKHCEPTFQSVK 314

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: A\_Geneseq\_21:\*  
2: geneeqp1980s:\*  
3: geneeqp1990s:\*  
4: geneeqp2000s:\*  
5: geneeqp2001s:\*  
6: geneeqp2002s:\*  
7: geneeqp2003as:\*  
8: geneeqp2004s:\*  
9: geneeqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1706	100.0	314	2	AAW88528 Human Frl
2	1706	100.0	314	6	ABP72783 Human sFR
3	1706	100.0	314	8	ADP68536 Human sec
4	1706	100.0	314	8	ADP68536 Human sec
5	1701	99.7	314	6	AAW37817 Human sec
6	1701	99.7	314	6	ABP72785 Human sec
7	1691.5	99.2	313	4	AAE10154 Human sec
8	1691.5	99.2	313	4	AAU07695 Human Frl
9	1691.5	99.2	313	6	ABP72784 Human sec
10	1691.5	99.2	313	7	ABR61428 Human emb
11	1691.5	99.2	313	8	ADP68541 Human sec
12	1691.5	99.2	313	8	ADU86503 Human sec
13	1691.5	99.2	313	8	AEA64566 Human lyp
14	1691.5	99.2	313	9	ADV44810 Secreted
15	1691.5	99.2	313	9	ADX58916 Human reg
16	1691.5	99.2	313	5	ABR61428 Human sec
17	1657.5	97.2	313	7	ADP68541 Human sec
18	1657.5	97.2	313	8	ADH43308 Human sec
19	1657.5	97.2	338	5	ABR61428 Human sec
20	1657.5	97.2	338	7	ADP68541 Human sec
21	1657.5	97.2	338	8	ADH43309 Human sFR
22	1634	95.8	362	8	ABR61429 Human dia
23	1634	95.8	362	8	ABR61429 Human dia
24	1623	95.1	314	7	ABR61427 Murine em

25	1623	95.1	314	8	ADU86506	Adu86506 Mouse sec
26	1267.5	74.3	267	5	ABR62248	Abbr62248 Human sec
27	1267.5	74.3	267	7	ADH43312	Adh43312 Deletion
28	1267.5	74.3	267	8	ADH43312	Adh43312 Human sec
29	1171	68.6	246	5	ABR62247	Abbr62247 Human sec
30	1171	68.6	246	7	ADH43311	Adh43311 Deletion
31	1171	68.6	246	8	ADH43311	Adh43311 Human sec
32	1155	67.7	381	6	ABU55906	Abu55906 Human sec
33	1155	67.7	381	6	ABU55918	Abu55918 Human sec
34	1155	67.7	381	6	AAE34072	Aae34072 SRF 1 pr
35	1155	67.7	381	6	AAE34060	Aae34060 Frl prote
36	971	56.9	229	5	ABR62249	Abbr62249 Human sec
37	971	56.9	229	7	ADH43313	Adh43313 Deletion
38	971	56.9	229	8	ADH43313	Adh43313 Human sec
39	924.5	54.2	317	6	AAW37816	Aaw37816 Human sec
40	924.5	54.2	317	6	ADH43289	Adh43289 Human sec
41	924.5	54.2	317	8	ADH43289	Adh43289 Human hom
42	924.5	54.2	317	8	ADP68542	ADP68542 Human PRO
43	922.5	54.1	314	6	ADH438292	Adh438292 Mouse sec
44	922.5	54.1	314	8	ADH438292	Adh438292 Murine ad
45	917.5	53.8	317	2	AAW73507	Aaw73507 Human ATG

## ALIGNMENTS

RESULT 1  
AAW88528 standard; protein; 314 AA.

AAW88528; 11-MAR-1999 (first entry)

Human Frlzled-related protein (FRP).

FRP, frizzled-related protein; human; Wnt binding domain; recombinant; cytokine; cell growth; differentiation; migration; tumour suppressor; oncogene(s); cancer; Drosophila; Wntless protein; Wnt; neoplasia; transgenic; therapeutic.

XX Homo sapiens.

XX Location/Qualifiers

XX Key 1.28 /note= "putative signal sequence"

XX Peptide 14 /note= "encoded by a CAG insertion sequence observed in some cDNA constructs"

XX Protein 29.314 /note= "mature protein"

XX Domain 57.166 /note= "Wnt binding domain"

XX Modified-site 173.175 /note= "Asn is potentially N-glycosylated"

XX Modified-site 263.265 /note= "Asn is potentially N-glycosylated"

XX W09854325-A1.

XX 03-DEC-1998.

XX 29-MAY-1998; 98WO-US010974.

XX 29-MAY-1997; 97US-0050417P.

XX 23-JUN-1997; 97US-0050495P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Rubin JS, Finch P, Aaronson S, He X;

XX WPI: 1999-059840/05.

XX N-PSDB; AAW84395.

DR

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OM protein - protein search, using sw model

Run on: May 5, 2006, 13:59:36 ; Search time 27 Seconds  
(without alignments)  
538.274 Million cell updates/sec

Title: US-10-666-851-2  
Perfect score: 1706  
Sequence: 1 MGGRSGRGRGAALGVLLA.....KNFMKMKHCEPTQSVFK 314

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA New:  
1: /SIDS5/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:.\*  
2: /SIDS5/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:.\*  
3: /SIDS5/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:.\*  
4: /SIDS5/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:.\*  
5: /SIDS5/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:.\*  
6: /SIDS5/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:.\*  
7: /SIDS5/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:.\*  
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9: /SIDS5/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:.\*  
10: /SIDS5/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:.\*  
11: /SIDS5/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:.\*  
12: /SIDS5/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1691.5	99.2	413	9	US-10-821-234-989 Sequence 989, App
2	605.5	35.5	295	11	US-11-067-121-2 Sequence 2, Appl
3	602	35.3	295	11	US-11-067-121-11 Sequence 11, Appl
4	602	35.3	295	11	US-11-051-720-1701 Sequence 1701, Ap
5	598	35.1	295	9	US-10-216-161A-415 Sequence 415, App
6	389.5	22.8	180	11	US-11-051-720-1306 Sequence 1306, Ap
7	298	17.5	117	11	US-11-054-281-306 Sequence 306, App
8	290	17.0	586	11	US-11-054-281-93 Sequence 93, Appl
9	280	16.4	530	11	US-11-054-281-94 Sequence 94, Appl
10	271.5	15.9	537	8	US-10-511-937-2607 Sequence 2607, Ap
11	271.5	15.9	537	11	US-11-152-366-43 Sequence 43, Appl
12	271.5	15.9	537	11	US-11-169-041-132 Sequence 132, App
13	271.5	15.9	537	11	US-11-169-041-134 Sequence 134, Appl
14	268.5	15.7	580	11	US-11-054-281-95 Sequence 95, Appl
15	267.5	15.7	592	11	US-11-054-281-127 Sequence 127, Appl
16	266.5	15.6	585	11	US-11-054-281-92 Sequence 92, Appl
17	262	15.4	591	11	US-11-054-281-36 Sequence 36, Appl
18	261.5	15.3	591	11	US-11-054-281-128 Sequence 128, App
19	259.5	15.2	188	11	US-11-152-366-249 Sequence 249, Appl
20	258	15.1	352	11	US-11-054-281-126 Sequence 126, Appl
21			319	11	US-11-184-005-7 Sequence 7, Appl

22	256.5	15.0	581	11	US-11-067-231-153 Sequence 153, App
23	256.5	15.0	581	11	US-11-054-281-22 Sequence 22, Appl
24	256.5	15.0	581	11	US-11-054-281-91 Sequence 91, Appl
25	253.5	14.9	325	11	US-11-184-005-2 Sequence 2, Appl
26	251	14.7	577	11	US-11-054-281-130 Sequence 130, App
27	248	14.5	319	11	US-11-184-005-8 Sequence 8, Appl
28	247.5	14.5	325	11	US-11-184-005-4 Sequence 4, Appl
29	244	14.3	111	11	US-11-184-005-5 Sequence 5, Appl
30	243	14.2	111	11	US-11-184-005-6 Sequence 6, Appl
31	243	14.2	549	11	US-11-054-281-129 Sequence 129, App
32	237	13.9	346	11	US-11-054-281-97 Sequence 97, Appl
33	236	13.8	348	11	US-11-054-281-69 Sequence 69, Appl
34	236	13.8	348	11	US-11-054-281-98 Sequence 98, Appl
35	235.5	13.8	351	11	US-11-054-281-100 Sequence 100, App
36	234.5	13.7	585	11	US-11-127-877-63 Sequence 63, Appl
37	234	13.7	348	11	US-11-054-281-99 Sequence 99, Appl
38	233	13.7	346	10	US-11-301-554-328 Sequence 329, App
39	233	13.7	346	11	US-11-186-284-189 Sequence 189, Appl
40	233	13.7	346	11	US-11-054-281-24 Sequence 24, Appl
41	233	13.7	346	11	US-11-054-281-96 Sequence 96, Appl
42	201	11.8	1113	11	US-11-067-811-4 Sequence 4, Appl
43	194	11.4	1042	11	US-11-067-811-1 Sequence 1, Appl
44	137.5	8.1	116	11	US-11-152-366-283 Sequence 283, App
45	137.5	8.1	433	11	US-11-152-366-44 Sequence 44, Appl

#### ALIGNMENTS

RESULT 1  
US-10-821-234-989  
Sequence 989, Application US/10821234  
Publication No. US20050255114A1  
GENERAL INFORMATION:  
APPLICANT: Labat, Ivan  
APPLICANT: Steche-Crain, Birgit  
APPLICANT: Andarmant, Susan  
APPLICANT: Tang, Y. Tom  
TITLE OR INVENTION: Methods for diagnosis and treatment of Preeclampsia  
FILE REFERENCE: 821A  
CURRENT APPLICATION NUMBER: US/10/821,234  
CURRENT FILING DATE: 2004-04-07  
PRIOR APPLICATION NUMBER: US 60/462,047  
PRIOR FILING DATE: 2003-04-07  
NUMBER OF SEQ ID NOS: 1704  
SOFTWARE: pc\_seq\_genes Version 1.0  
SEQ ID NO 989  
LENGTH: 413  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-821-234-989

Query Match 99.2% Score 1691.5; DB 9; Length 413;  
Best Local Similarity 99.7% Pred. No. 1e-152;  
Matches 313; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY	1	MGGRSGRGRGAALGVLLAAGNALAVGSASDYVSPQSDIGPYQSGFTRKPPQCV	60
DB	101	MGGRSGRGRGRG-ALGVLLALAGNALAVGSASDYVSPQSDIGPYQSGFTRKPPQCV	159
QY	61	IPADLRLCHNVGKRVNLPVLEHETMAVYKQDASSMVPPLANKNCHAGTQVPLCSHFAV	120
DB	160	IPADLRLCHNVGKRVNLPVLEHETMAVYKQDASSMVPPLANKNCHAGTQVPLCSHFAV	219
QY	121	CLDRPYPCRMVCEAVRDSCEPVMQFPGTYPMKCDKDFPBGDVCIANTPPNATASRP	180
DB	220	CLDRPYPCRMVCEAVRDSCEPVMQFPGTYPMKCDKDFPBGDVCIANTPPNATASRP	279
QY	181	OGTTVPCCDNLKSAITIEHLCASEFALRMKIKVYKKNQDKKIVPKKKKPKLGLPIRK	240
DB	280	OGTTVPCCDNLKSAITIEHLCASEFALRMKIKVYKKNQDKKIVPKKKKPKLGLPIRK	339
QY	241	KDKKLVLYLKGADPCHQDLNLSHHPLIMGRKVSQYLLTAIHRMCKKXKPFKNFMKK	300





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OM protein - protein search, using sw model

Run on: May 5, 2006, 13:58:01 ; Search time 46 Seconds  
(without alignments)  
564.351 Million cell updates/sec

Title: US-10-666-851-2

Perfect score: 1706

Sequence: 1 MEIGRSGGRRGALGVLLA.....KNFMKKMKHCEPTQSVK 314

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/prodata/1/aa/5 COMB.pep:\*  
2: /cgn2\_6/prodata/1/aa/6 COMB.pep:\*  
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4: /cgn2\_6/prodata/1/aa/PC/US COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1701	99.7	314	2	US-08-937-067-7 Sequence 7, Appl
2	1691.5	99.2	313	2	US-09-514-885-1 Sequence 1, Appl
3	1691.5	99.2	313	2	US-09-949-016-6299 Sequence 6299, Ap
4	1657.5	97.2	313	2	US-09-546-043-3 Sequence 3, Appl
5	1657.5	97.2	338	2	US-09-546-043-4 Sequence 4, Appl
6	1629	95.5	314	2	US-09-087-031B-3 Sequence 3, Appl
7	1614.5	94.6	313	2	US-09-087-031B-4 Sequence 4, Appl
8	1267.5	74.3	267	2	US-09-546-043-7 Sequence 7, Appl
9	1171	68.6	246	2	US-09-546-043-6 Sequence 6, Appl
10	971	56.9	229	2	US-08-546-043-8 Sequence 8, Appl
11	924.5	54.2	317	2	US-08-937-067-6 Sequence 6, Appl
12	924.5	54.2	317	2	US-09-949-016-6300 Sequence 6300, Ap
13	911.5	53.4	305	2	US-09-949-016-7706 Sequence 7706, Ap
14	887.5	52.0	195	2	US-09-546-043-5 Sequence 5, Appl
15	805.5	35.5	295	2	US-08-937-067-2 Sequence 2, Appl
16	598	35.1	295	2	US-09-999-833A-415 Sequence 415, App
17	598	35.1	295	2	US-10-020-445A-415 Sequence 415, App
18	597	35.0	295	2	US-09-148-545-179 Sequence 179, App
19	597	35.0	295	2	US-09-621-011-179 Sequence 179, App
20	597	35.0	295	2	US-09-148-545-237 Sequence 237, App
21	597	35.0	296	2	US-09-621-011-237 Sequence 237, App
22	594	34.8	109	2	US-09-087-031B-19 Sequence 19, Appl
23	508.5	29.8	295	2	US-08-893-654B-6 Sequence 6, Appl
24	436	25.6	212	2	US-08-937-067-4 Sequence 4, Appl
25	409.5	24.0	280	2	US-08-893-654B-4 Sequence 4, Appl
26	387	22.7	281	2	US-08-893-654B-2 Sequence 2, Appl
27	353	20.7	113	2	US-09-087-031B-24 Sequence 24, Appl

28	272.5	16.0	572	2	US-08-937-067-13 Sequence 13, Appl
29	262.5	15.4	537	2	US-08-937-067-11 Sequence 11, Appl
30	262	15.4	319	2	US-10-014-055-7 Sequence 7, Appl
31	258	15.1	318	2	US-10-014-055-8 Sequence 8, Appl
32	258	15.1	319	2	US-10-028-051A-7 Sequence 7, Appl
33	258	15.1	319	2	US-08-937-067-8 Sequence 8, Appl
34	253.5	14.9	325	2	US-10-014-055-2 Sequence 2, Appl
35	253.5	14.9	325	2	US-10-028-051A-2 Sequence 2, Appl
36	252	14.8	318	2	US-08-878-474-3 Sequence 3, Appl
37	248	14.5	319	2	US-10-028-051A-8 Sequence 8, Appl
38	247.5	14.5	323	2	US-08-878-474-7 Sequence 7, Appl
39	247.5	14.5	325	2	US-08-878-474-9 Sequence 9, Appl
40	247.5	14.5	325	2	US-09-976-594-479 Sequence 479, App
41	247.5	14.5	325	2	US-10-014-055-4 Sequence 4, Appl
42	247.5	14.5	325	2	US-10-028-051A-4 Sequence 4, Appl
43	247.5	14.5	371	2	US-09-849-016-7544 Sequence 7544, Ap
44	244	14.3	111	2	US-10-014-055-5 Sequence 5, Appl
45	244	14.3	111	2	US-10-028-051A-5 Sequence 5, Appl

#### ALIGNMENTS

RESULT 1  
US-08-937-067-7  
Sequence 7, Application US/08937067  
Patent No. 6433155

GENERAL INFORMATION:

APPLICANT: Umanaky, Samu1

TITLE OF INVENTION: Melkonyan, Hovsep

TITLE OF INVENTION: A FAMILY OF GENES ENCODING APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND

TITLE OF INVENTION: METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FORSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,067

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 314 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-937-067-7

Query Match 99.7%; Score 1701; DB 2; Length 314;  
Best Local Similarity 99.7%; Pred. No. 3.5e-174;  
Matches 313; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 MEIGRSGGRRGALGVLLAAGALLAVGASAEVDYVSFSDIGPGVSGRFTYKPPQVD 60

GenCore version 5.1.7  
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OM protein - protein search, using SW model

Run on: May 5, 2006, 14:09:22 ; Search time 29 Seconds  
(without alignments)  
42.763 Million cell updates/sec

Title: US-10-666-851-2\_COPY\_217\_231  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues  
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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	78	100.0	267	US-09-546-043-7	Sequence 7, App11
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4	78	100.0	313	US-09-546-043-3	Sequence 3, App11
5	78	100.0	313	US-09-514-885-1	Sequence 1, App11
6	78	100.0	313	US-09-949-016-6299	Sequence 6299, App
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8	78	100.0	314	US-09-087-0318-3	Sequence 3, App11
9	78	100.0	338	US-09-546-043-4	Sequence 4, App11
10	53	67.9	108	US-09-319-588C-6	Sequence 6, App11
11	46	59.0	1014	US-09-949-016-7706	Sequence 7706, App
12	45	57.7	305	US-08-937-067-6	Sequence 6, App11
13	45	57.7	317	US-09-949-016-6300	Sequence 6300, App
14	45	57.7	317	US-09-206-551-46	Sequence 46, App11
15	45	57.7	334	US-09-248-796A-16963	Sequence 16963, A
16	44	56.4	144	US-09-107-433-3451	Sequence 3451, A
17	43	55.1	316	US-09-270-767-34052	Sequence 34052, A
18	43	55.1	316	US-09-270-767-49269	Sequence 49269, A
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21	42	53.8	177	US-09-248-796A-14797	Sequence 14797, A
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57	40	51.3	913	1	US-07-743-357-6	Sequence 6, App11
58	40	51.3	913	1	US-07-743-357-7	Sequence 7, App11
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61	40	51.3	1002	2	US-10-290-579A-189	Sequence 189, App
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87	39	50.0	59	2	US-09-621-976-5183	Sequence 5183, App
88	39	50.0	63	2	US-09-248-796A-21747	Sequence 21747, A
89	39	50.0	71	2	US-09-621-976-5184	Sequence 5184, App
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91	39	50.0	78	1	US-07-991-867B-4	Sequence 4, App11
92	39	50.0	78	1	US-08-107-755A-4	Sequence 4, App11
93	39	50.0	78	1	US-08-544-332-4	Sequence 4, App11
94	39	50.0	78	1	US-09-370-861B-4	Sequence 4, App11
95	39	50.0	85	2	US-09-733-685-10	Sequence 10, App11
96	39	50.0	85	2	US-09-513-999C-5823	Sequence 5823, App
97	39	50.0	103	2	US-09-564-329A-11	Sequence 11, App11
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GenCore version 5.1.7  
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57.856 Million cell updates/sec

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Searched: 235405 seqs, 46284737 residues

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Post-processing: Minimum Match 0%  
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Listing first 500 summaries

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4: /SIDS5/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	100.0	413	9	US-10-821-234-989
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6	42	53.8	540	11	US-11-087-099-4162
7	42	53.8	541	11	US-11-087-099-2152
8	41	52.6	263	11	US-11-079-463-8502
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11	41	52.6	409	9	US-10-533-811-57
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13	41	52.6	474	11	US-11-096-568A-21505
14	41	52.6	544	11	US-11-096-568A-21504
15	41	52.6	545	11	US-11-087-099-951
16	41	52.6	547	11	US-11-087-099-3034
17	41	52.6	723	11	US-11-045-004-1839
18	40	51.3	35	11	US-11-096-725-1
19	40	51.3	259	11	US-11-079-463-6740
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39	38	48.7	17	11	US-11-171-567-117	Sequence 117, App
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46	38	48.7	154	11	US-11-096-568A-25432	Sequence 25432, A
47	38	48.7	191	11	US-11-188-298-19979	Sequence 19979, A
48	38	48.7	260	11	US-11-079-463-6738	Sequence 6738, App
49	38	48.7	511	11	US-11-096-568A-29784	Sequence 29784, A
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51	38	48.7	674	11	US-11-096-568A-29783	Sequence 29783, A
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53	37	47.4	113	11	US-11-045-024-3443	Sequence 3443, App
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55	37	47.4	11	11	US-11-045-024-11863	Sequence 11863, A
56	37	47.4	51	11	US-11-096-568A-10067	Sequence 10067, A
57	37	47.4	62	11	US-11-096-568A-4419	Sequence 4419, App
58	37	47.4	78	11	US-11-096-568A-4418	Sequence 4418, App
59	37	47.4	111	11	US-11-079-463-9706	Sequence 9706, App
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71	37	47.4	295	11	US-11-096-568A-34149	Sequence 34149, A
72	37	47.4	335	11	US-11-096-568A-34148	Sequence 34148, A
73	37	47.4	335	11	US-11-096-568A-34147	Sequence 34147, A
74	37	47.4	361	11	US-11-096-568A-34562	Sequence 32562, A
75	37	47.4	365	11	US-11-096-568A-32561	Sequence 32561, A
76	37	47.4	392	11	US-11-096-568A-32560	Sequence 32560, A
77	37	47.4	408	11	US-11-188-298-17882	Sequence 17882, A
78	37	47.4	430	11	US-11-126-313-35	Sequence 35, App1
79	37	47.4	430	11	US-11-126-313-36	Sequence 36, App1
80	37	47.4	504	11	US-11-087-099-1103	Sequence 1053, App
81	37	47.4	554	11	US-11-098-686-11102	Sequence 11102, A
82	37	47.4	560	11	US-11-087-099-5820	Sequence 5820, App
83	37	47.4	851	8	US-10-511-937-2597	Sequence 2597, App
84	37	47.4	1078	11	US-11-169-041-205	Sequence 205, App
85	37	47.4	1078	11	US-11-096-568A-30451	Sequence 30451, A
86	37	47.4	1116	11	US-11-096-568A-30450	Sequence 30450, A
87	37	47.4	1116	11	US-11-096-568A-30449	Sequence 30449, A
88	37	47.4	1110	11	US-11-086-482-1	Sequence 1, App1
89	37	47.4	1130	11	US-11-192-341-23	Sequence 23, App1
90	37	47.4	2344	9	US-10-330-773-627	Sequence 627, App
91	37	47.4	2801	9	US-10-330-773-630	Sequence 630, App
92	36.5	46.8	954	11	US-11-079-463-10024	Sequence 10024, A
93	36	46.2	124	11	US-11-172-740-1758	Sequence 1758, App
94	36	46.2	155	11	US-11-072-512-3937	Sequence 3937, App

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# OM protein - protein search, using sw model

Run on: May 5, 2006, 14:06:21 / Search time 38 Seconds  
(without alignments)  
37.980 Million cell updates/sec

Title: US-10-666-851-2\_COPY\_217\_231  
Perfect score: 78  
Sequence: 1 KKEKNGDKIIVPKKKK 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 500 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	59.0	205	2 T20980	hypothetical prote
2	46	59.0	279	2 T20987	hypothetical prote
3	46	59.0	397	2 T20013	hypothetical prote
4	46	59.0	3488	2 T34418	hypothetical prote
5	45	57.7	65	2 C69792	hypothetical prote
6	45	57.7	317	2 J80175	freezied protein-1
7	44	56.4	502	2 T22045	hypothetical prote
8	43.5	55.8	502	2 T14286	embryogenic callus
9	43	55.1	132	2 T48278	hypothetical prote
10	43	55.1	175	2 T05669	hypothetical prote
11	43	55.1	245	2 T50399	hypothetical prote
12	43	55.1	690	2 E72337	translaction initia
13	43	55.1	1196	2 T23832	protein-tyrosine k
14	43	55.1	1278	2 A71609	probable secreted
15	42	53.8	95	2 G97706	hypothetical prote
16	42	53.8	183	2 A35270	ribosomal protein
17	42	53.8	288	2 S26495	transcription fact
18	42	53.8	295	2 B86371	hypothetical prote
19	42	53.8	367	2 T39172	cyclin-dependent k
20	42	53.8	625	2 A90127	hypothetical prote
21	42	53.8	734	2 T23647	DNA topoisomerase
22	42	53.8	751	2 S65469	hypothetical prote
23	42	53.8	806	2 T23648	hypothetical prote
24	42	53.8	881	2 T49279	hypothetical prote
25	42	53.8	1063	2 T38732	probable helicase
26	42	53.8	2441	2 D71623	erythrocyte membra
27	41.5	53.2	239	2 A98291	hypothetical prote
28	41.5	53.2	422	2 G90259	hypothetical prote
29	41.5	53.2	422	2 H90271	hypothetical prote

30	41.5	53.2	422	2 H90275	hypothetical prote
31	41	52.6	109	2 A86505	l31 ribosomal prot
32	41	52.6	109	2 H72118	ribosomal protein
33	41	52.6	115	2 S01281	hypothetical prote
34	41	52.6	200	2 B95057	hypothetical prote
35	41	52.6	200	2 B97926	rNA polymerase (de
36	41	52.6	224	2 T39771	hypothetical prote
37	41	52.6	277	2 D97067	probable xyJanase/
38	41	52.6	285	2 T27458	hypothetical prote
39	41	52.6	399	2 T32933	cell-divislon prot
40	41	52.6	400	2 AB1565	6-phosphogluconate
41	41	52.6	472	2 AH1246	hypothetical prote
42	41	52.6	472	2 AD1509	hypothetical prote
43	41	52.6	539	2 T23526	hypothetical prote
44	41	52.6	552	2 S48328	hypothetical prote
45	41	52.6	648	2 T27412	polynucleotide pho
46	41	52.6	723	2 AC1241	polynucleotide pho
47	41	52.6	723	2 AG1603	ribonucleotide red
48	41	52.6	763	2 H97302	DNA topoisomerase
49	41	52.6	769	1 ISBT1	hypothetical prote
50	41	52.6	1359	2 T34036	hypothetical prote
51	40.5	51.9	422	2 H90501	pol polypotein -
52	40	51.3	44	2 T09381	histone H2B-8 - wh
53	40	51.3	78	1 P64061	pol polypotein -
54	40	51.3	138	2 S56685	hypothetical prote
55	40	51.3	148	2 A26192	hypothetical prote
56	40	51.3	155	2 H96761	p22L4.5 protein -
57	40	51.3	203	2 F86145	hypothetical prote
58	40	51.3	235	2 AD1735	hypothetical prote
59	40	51.3	251	2 T39332	hypothetical prote
60	40	51.3	278	2 S67432	pol lipoprotein dia
61	40	51.3	289	2 B84098	hypothetical prote
62	40	51.3	427	2 T41257	hypothetical prote
63	40	51.3	504	2 D71615	hypothetical prote
64	40	51.3	521	2 T16692	hypothetical prote
65	40	51.3	522	2 C96608	probable NADH2 deh
66	40	51.3	820	2 C81252	hypothetical prote
67	40	51.3	839	2 T16753	pol polypotein -
68	40	51.3	902	2 T01668	pol polypotein -
69	40	51.3	912	2 S33980	pol polypotein -
70	40	51.3	1002	1 GNLJND	pol polypotein -
71	40	51.3	1002	2 S54378	HIV-1 retropepsin
72	40	51.3	1003	1 GNMWLV	HIV-1 retropepsin
73	40	51.3	1003	1 B44001	HIV-1 retropepsin
74	40	51.3	1003	2 T09440	pol polypotein -
75	40	51.3	1003	2 GNMWLV	HIV-1 retropepsin
76	40	51.3	1012	1 GNMWLV	HIV-1 retropepsin
77	40	51.3	1015	1 GNMWLV	DNA topoisomerase
78	40	51.3	1447	2 S02160	multidrug resistanc
79	40	51.3	1545	1 S71841	calcium channel pr
80	40	51.3	1851	2 T13980	cell proliferation
81	40	51.3	2515	2 A41519	Gli protein - Amas
82	40	51.3	2938	2 T30249	hypothetical prote
83	39	50.0	78	1 WZVZG3	histone H2B - whea
84	39	50.0	101	2 G90536	transcription regu
85	39	50.0	152	2 S22353	transcription regu
86	39	50.0	169	2 AD3110	hypothetical prote
87	39	50.0	179	2 S61904	transcription regu
88	39	50.0	201	2 H98176	hypothetical prote
89	39	50.0	205	2 T00865	hypothetical prote
90	39	50.0	226	2 S41032	ribosomal protein
91	39	50.0	277	2 AB1403	hypothetical prote
92	39	50.0	277	2 AD1779	hypothetical prote
93	39	50.0	298	2 G96773	hypothetical prote
94	39	50.0	321	2 T39278	hypothetical prote
95	39	50.0	392	2 T19327	protein p22C12.16
96	39	50.0	411	2 B96665	transcription init
97	39	50.0	425	2 S76760	hypothetical prote
98	39	50.0	491	2 T21421	protein-tyrosine-p
99	39	50.0	535	2 A46101	probable U4/U6 sma
100	39	50.0	542	2 S62508	protein-tyrosine-p
101	39	50.0	548	2 B46101	hypothetical prote
102	39	50.0	557	2 T04465	hypothetical prote

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## OM protein - protein search, using sw model

Run on: May 5, 2006, 14:02:56 ; Search time 226 Seconds  
(without alignments)  
46.827 Million cell updates/sec

Title: US-10-666-851-2\_COPY\_217\_231  
Perfect score: 78  
Sequence: 1 KKENSGDKKIVPKKKK 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : Uniprot 05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	100.0	158	1	SRP1_RAT
2	78	100.0	178	1	06ZSL4_HUMAN
3	78	100.0	308	1	SRP1_BOVIN
4	78	100.0	314	1	SRP1_HUMAN
5	78	100.0	314	1	SRP1_MOUSE
6	78	100.0	314	2	0505A2_MOUSE
7	64	82.1	314	1	SRP1_CHICK
8	58	74.4	5229	2	Q7RTP4_PLYAO
9	51	65.4	536	2	Q64CC4_PANCA
10	50	64.1	311	2	Q9Y124_XENLA
11	49	62.8	287	2	Q614B0_CABER
12	49	62.8	308	2	050YPS_ENTHI
13	49	62.8	326	2	050OP4_ENTHI
14	49	62.8	758	2	Q4RUV9_TETNG
15	48	61.5	310	2	Q6YNR8_BRARE
16	48	61.5	321	2	Q4SKX3_TETNG
17	47	60.3	297	2	Q82W10_NITRU
18	47	60.3	348	2	Q7RA45_PLYAO
19	47	60.3	425	2	Q4YPAB_PLAAB
20	47	60.3	610	2	Q9LIH8_ARATH
21	46	59.0	166	2	Q9WIS8_SHIV1
22	46	59.0	261	2	Q4Y8S7_PLACH
23	46	59.0	278	2	Q814L0_CABER
24	46	59.0	279	1	Y611_CABER
25	46	59.0	286	2	Q909N2_SHIV1
26	46	59.0	315	2	Q8AWG4_XENLA
27	46	59.0	315	2	Q640J3_XENLA
28	46	59.0	315	2	Q6GL50_XENTR
29	46	59.0	324	2	Q54Q96_DICDI
30	46	59.0	377	2	Q4Z5H0_PLAAB
31	46	59.0	397	1	YXX7_CABER

32	46	59.0	441	2	Q58EAB_BRARE
33	46	59.0	510	2	Q4V7X3_XENLA
34	46	59.0	532	2	Q9W600_XENLA
35	46	59.0	713	2	Q6PAX0_XENLA
36	46	59.0	715	2	Q4Y8S2_PLACH
37	46	59.0	725	2	Q965E8_ENTHI
38	46	59.0	819	2	Q54UR9_DICDI
39	46	59.0	912	2	Q6KER9_SHIV1
40	46	59.0	999	2	Q4J336_SHIV1
41	46	59.0	1002	2	Q8USZ3_SHIV1
42	46	59.0	1003	2	Q8JBU7_SHIV1
43	46	59.0	1010	2	Q5K5U6_SHIV2
44	46	59.0	1011	2	Q8U7F1_SHIV1
45	46	59.0	1012	2	Q673V0_SHIV1
46	46	59.0	1069	2	Q519R3_ENTHI
47	46	59.0	1080	2	Q510Y4_ENTHI
48	46	59.0	1431	2	Q8AE72_SHIV1
49	46	59.0	1433	2	Q91R69_SHIV1
50	46	59.0	1449	2	Q910B0_SHIV1
51	46	59.0	1449	2	Q91DV9_SHIV1
52	46	59.0	18519	2	Q8ISF6_CABER
53	46	59.0	18534	2	Q8ISF7_CABER
54	46	57.7	65	2	Q34700_BACSU
55	46	57.7	84	2	Q4TF10_TETNG
56	46	57.7	184	2	Q7VVG5_BORPE
57	45	57.7	194	2	Q7MAE5_BORPA
58	45	57.7	194	2	Q7WJ18_BORPA
59	45	57.7	213	2	Q4UR09_TREAN
60	45	57.7	315	1	SRP5_BOVIN
61	45	57.7	317	1	SRP5_HUMAN
62	45	57.7	350	2	Q7RAP6_PLYAO
63	45	57.7	418	2	Q4S674_TETNG
64	45	57.7	493	2	Q9SUI9_ARATH
65	45	57.7	574	2	Q55C31_DICDI
66	45	57.7	577	2	Q7YZJ2_SMERT
67	45	57.7	630	2	Q4YN70_PLAAB
68	45	57.7	699	2	Q5FXS8_SHIV1
69	45	57.7	714	2	Q7RG16_PLYAO
70	45	57.7	1055	2	Q4XXY6_PLAAB
71	45	57.7	1089	2	Q75B21_ASHGO
72	45	57.1	289	2	Q4YTF4_PLAAB
73	44.5	57.1	317	2	Q4Y76 PLAB
74	44.5	57.1	516	2	Q6AL1 DESPS
75	44	56.4	273	2	Q5AP68_CANAL
76	44	56.4	278	2	Q8D2B4_WIGBR
77	44	56.4	281	2	Q568X0_BRARE
78	44	56.4	296	2	Q72K9 BRARE
79	44	56.4	335	2	Q9BLU5_ACPY1
80	44	56.4	377	1	DNAJ_STR1
81	44	56.4	377	1	DNAJ_STR2
82	44	56.4	476	2	Q4X16 PLACH
83	44	56.4	502	2	Q20240_CABER
84	44	56.4	562	2	Q90038_VITRU
85	44	56.4	587	2	Q59X38_CANAL
86	44	56.4	637	2	Q5TXQ0_ANOGA
87	44	56.4	659	2	Q6BK6 DEBHA
88	44	56.4	690	2	Q7PCN5_ANOGA
89	44	56.4	743	2	Q6P1W7_HUMAN
90	44	56.4	868	2	Q503P4_BRARE
91	44	56.4	919	2	Q7Q942_ANOGA
92	44	56.4	972	2	Q5TSL5_ANOGA
93	44	56.4	1003	2	Q69G76_SHIV1
94	44	56.4	1003	2	Q69G87_SHIV1
95	44	56.4	1476	2	Q5G8Z4_XENLA
96	44	56.4	2378	2	Q813U0_PLYAF
97	44	56.4	4261	2	Q81FP4_PLYAF
98	43.5	55.8	502	2	Q803B3_DAUCA
99	43	55.1	61	2	Q811Q8_PLYAF
100	43	55.1	120	2	Q95XHA_CABER
101	43	55.1	127	2	Q4J7N1_SULAC
102	43	55.1	132	2	Q9LZ45_ARATH
103	43	55.1	163	2	Q8G117_ARATH
104	43	55.1	175	2	Q9SVE4_ARATH

Q58EAB	brachydantio
Q4V7X3	xenopus lae
Q9W600	xenopus lae
Q6PAX0	xenopus lae
Q4Y8S2	plasmodium
Q965E8	entamoeba h
Q54UR9	dictyostell
Q6KER9	human immun
Q4J336	human immun
Q8USZ3	human immun
Q8JBU7	human immun
Q5K5U6	chimpanzee
Q8U7F1	human immun
Q673V0	human immun
Q519R3	entamoeba h
Q510Y4	entamoeba h
Q8AE72	human immun
Q91R69	human immun
Q910B0	human immun
Q91DV9	human immun
Q8ISF6	caenorhabdi
Q8ISF7	caenorhabdi
Q34700	bacillus su
Q4TF10	tetradodon n
Q7VVG5	bordetella
Q7MAE5	bordetella
Q7WJ18	bordetella
Q4UR09	shelleria a
SRP5_BOVIN	bov taurus
SRP5_HUMAN	homo sapien
Q7RAP6	plasmodium
Q4S674	tetradodon n
Q9SUI9	arabidopsis
Q55C31	dictyostell
Q7YZJ2	halichondri
Q4YN70	plasmodium
Q5FXS8	human immun
Q7RG16	plasmodium
Q4XXY6	plasmodium
Q75B21	ashbya gos
Q4YTF4	plasmodium
Q4Y76	plasmodium
Q6AL1	desulfofale
Q5AP68	candida alb
Q8D2B4	wiggleswort
Q568X0	brachydantio
Q72K9	brachydantio
Q9BLU5	acetylcholin
DNAJ_STR1	streplococc
DNAJ_STR2	streplococc
Q4X16	caenorhabdi
Q20240	caenorhabdi
Q90038	scabia virus
Q59X38	candida alb
Q5TXQ0	anopheles g
Q6BK6	debarjowce
Q7PCN5	anopheles g
Q6P1W7	homo sapien
Q503P4	brachydantio
Q7Q942	anopheles g
Q5TSL5	anopheles g
Q69G76	human immun
Q69G87	human immun
Q5G8Z4	xenopus lae
Q813U0	plasmodium
Q81FP4	plasmodium
Q803B3	dancus caro
Q811Q8	plasmodium
Q95XHA	caenorhabdi
Q4J7N1	bulfolobus
Q9LZ45	arabidopsis
Q8G117	arabidopsis
Q9SVE4	arabidopsis

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OM protein - protein search, using sw model

Run on: May 5, 2006, 14:10:03 / Search time 76 Seconds  
(without alignments)  
82.466 Million cell updates/sec

Title: US-10-666-851-2\_COPY\_217\_231  
Perfect score: 78  
Sequence: 1 KKENGDKKIVPKKKK 15

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1867569 reqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 500 summaries

Database : Published Applications AA Main:\*

- 1: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubppaa/US10a\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubppaa/US10b\_PUBCOMB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	141	4	US-10-466-136-13 Sequence 13, Appl
2	78	100.0	229	4	US-10-425-586-8 Sequence 8, Appl1
3	78	100.0	229	4	US-10-466-136-8 Sequence 8, Appl1
4	78	100.0	267	4	US-10-425-586-7 Sequence 7, Appl1
5	78	100.0	267	4	US-10-466-136-7 Sequence 7, Appl1
6	78	100.0	313	3	US-09-796-008-2 Sequence 2, Appl1
7	78	100.0	313	4	US-10-138-434A-4 Sequence 4, Appl1
8	78	100.0	313	4	US-10-425-586-3 Sequence 3, Appl1
9	78	100.0	313	4	US-10-466-136-3 Sequence 3, Appl1
10	78	100.0	313	4	US-10-666-851-7 Sequence 7, Appl1
11	78	100.0	313	4	US-10-786-720-43 Sequence 43, Appl1
12	78	100.0	313	5	US-10-817-525-2 Sequence 2, Appl1
13	78	100.0	313	5	US-10-847-972-77 Sequence 77, Appl1
14	78	100.0	314	4	US-10-146-474-7 Sequence 7, Appl1
15	78	100.0	314	4	US-10-138-434A-3 Sequence 3, Appl1
16	78	100.0	314	4	US-10-301-764-7 Sequence 7, Appl1
17	78	100.0	314	4	US-10-666-851-2 Sequence 2, Appl1
18	78	100.0	314	4	US-10-788-792-148 Sequence 148, Appl
19	78	100.0	314	4	US-10-847-972-80 Sequence 80, Appl1
20	78	100.0	314	5	US-10-756-149-5611 Sequence 5611, Ap
21	78	100.0	338	4	US-10-425-586-4 Sequence 4, Appl1
22	78	100.0	338	4	US-10-466-136-4 Sequence 4, Appl1
23	53	67.9	108	5	US-10-617-320-4788 Sequence 4788, Ap
24	50.5	64.1	114	4	US-10-424-599-210561 Sequence 210561,
25	50	64.1	83	4	US-10-425-115-230293 Sequence 230293,
26	50	64.1	153	4	US-10-425-115-231235 Sequence 231235,
27	49	62.8	66	4	US-10-425-115-277499 Sequence 277499,

28	48	61.5	78	4	US-10-425-115-243409 Sequence 243409,
29	47	60.3	89	4	US-10-437-963-126220 Sequence 126220,
30	47	60.3	100	4	US-10-425-115-203483 Sequence 203483,
31	47	60.3	105	4	US-10-425-115-238136 Sequence 238136,
32	47	60.3	106	4	US-10-425-115-276508 Sequence 276508,
33	47	60.3	158	4	US-10-425-115-165021 Sequence 165021,
34	47	60.3	165	4	US-10-425-115-207527 Sequence 207527,
35	46.5	59.6	66	4	US-10-425-115-267035 Sequence 267035,
36	46	59.0	48	4	US-10-425-115-208785 Sequence 208785,
37	46	59.0	82	4	US-10-425-115-201158 Sequence 201158,
38	46	59.0	90	4	US-10-425-115-276281 Sequence 276281,
39	46	59.0	1014	4	US-10-301-661A-6 Sequence 6, Appl1
40	45	57.7	64	4	US-10-425-115-223443 Sequence 223443,
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42	45	57.7	91	4	US-10-424-599-197216 Sequence 197216,
43	45	57.7	119	4	US-10-424-599-273759 Sequence 273759,
44	45	57.7	122	4	US-10-425-115-200729 Sequence 200729,
45	45	57.7	184	4	US-10-424-599-188977 Sequence 188977,
46	45	57.7	194	4	US-10-282-122A-51035 Sequence 51035, A
47	45	57.7	317	4	US-10-146-474-6 Sequence 6, Appl1
48	45	57.7	317	4	US-10-338-604-2 Sequence 2, Appl1
49	45	57.7	317	4	US-10-301-764-6 Sequence 6, Appl1
50	45	57.7	317	5	US-10-768-566-1 Sequence 1, Appl1
51	45	57.7	816	4	US-10-425-115-280739 Sequence 280739,
52	45	57.7	931	4	US-10-425-115-262142 Sequence 262142,
53	45	57.7	1018	4	US-10-369-294-46 Sequence 46, Appl1
54	45	56.4	43	4	US-10-424-599-148923 Sequence 148923,
55	44	56.4	44	4	US-10-425-115-341736 Sequence 341736,
56	44	56.4	53	4	US-10-437-963-124929 Sequence 124929,
57	44	56.4	65	4	US-10-424-599-236534 Sequence 236534,
58	44	56.4	65	4	US-10-424-599-164574 Sequence 164574,
59	44	56.4	66	4	US-10-425-115-208959 Sequence 208959,
60	44	56.4	68	4	US-10-424-599-231259 Sequence 231259,
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62	44	56.4	78	4	US-10-437-963-193907 Sequence 193907,
63	44	56.4	81	4	US-10-425-115-224408 Sequence 224408,
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65	44	56.4	85	4	US-10-437-963-182779 Sequence 182779,
66	44	56.4	114	4	US-10-767-701-552041 Sequence 552041, A
67	44	56.4	124	4	US-10-424-599-150171 Sequence 150171,
68	44	56.4	160	4	US-10-425-115-227125 Sequence 227125,
69	44	56.4	202	4	US-10-425-115-338001 Sequence 338001,
70	44	56.4	216	4	US-10-425-115-275569 Sequence 275569,
71	44	56.4	246	4	US-10-425-115-136903 Sequence 136903,
72	44	56.4	335	5	US-10-437-963-124505 Sequence 124505, Ap
73	44	56.4	587	4	US-10-032-585-7334 Sequence 7334, Ap
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96	43	55.1	125	4	US-10-425-115-286013 Sequence 286013,
97	43	55.1	144	5	US-10-617-320-3451 Sequence 3451, Ap
98	43	55.1	164	4	US-10-425-115-336591 Sequence 336591,
99	43	55.1	180	4	US-10-437-963-112626 Sequence 112626,
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## OM protein - protein search, using sw model

Run on: May 5, 2006, 14:02:26 ; Search time 184 Seconds  
(without alignments)  
35.819 Million cell updates/sec

Title: US-10-666-851-2\_COPY\_217\_231  
Perfect score: 78  
Sequence: 1 KKENGDKIVPKKK 15

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

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9: geneseqp2005s:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	100.0	141	5	ABR82254 Human sFR
2	78	100.0	148	5	AAY48493 Human bre
3	78	100.0	178	8	ADR09139 Human pro
4	78	100.0	229	5	ABR82249 Human sec
5	78	100.0	229	7	ADC71191 Deletion
6	78	100.0	229	8	ADH43313 Human sec
7	78	100.0	267	5	ABR82248 Human sec
8	78	100.0	267	7	ADC71190 Deletion
9	78	100.0	267	8	ADH43312 Human sec
10	78	100.0	313	4	AAE10154 Human sec
11	78	100.0	313	5	AAU07695 Human pri
12	78	100.0	313	5	ABR82244 Human sec
13	78	100.0	313	6	ABP72784 Human sec
14	78	100.0	313	7	ABR61428 Human emb
15	78	100.0	313	7	ADC71186 Human sec
16	78	100.0	313	8	ADH43308 Human sec
17	78	100.0	313	8	ADP68541 Human sec
18	78	100.0	313	8	ADU86503 Human sec
19	78	100.0	313	8	AEH64566 Human lyp
20	78	100.0	313	9	ADV44810 Secreted
21	78	100.0	313	9	ADX58916 Human reg
22	78	100.0	314	2	AAW37817 Human sec
23	78	100.0	314	2	AAW88528 Human pri
24	78	100.0	314	6	ABP72785 Human sec

25	78	100.0	314	6	ABP72783	ABP72783 Human sFR
26	78	100.0	314	7	ABR61429	ABR61429 Murine em
27	78	100.0	314	7	ABR61427	ABR61427 Murine em
28	78	100.0	314	8	ADP68536	ADP68536 Human sec
29	78	100.0	314	8	ADR99142	ADR99142 Secreted
30	78	100.0	314	8	ADU86506	ADU86506 Mouse sec
31	78	100.0	314	5	ABR82245	ABR82245 Human sec
32	78	100.0	318	7	ADC71187	ADC71187 Human sFR
33	78	100.0	338	8	ADH43309	ADH43309 Human sFR
34	78	100.0	352	8	ABR82799	ABR82799 Human dia
35	53	67.9	108	8	ADR96153	ADR96153 Novel S.
36	53	67.9	108	8	AEA60023	AEA60023 Strepto
37	49	62.8	110	4	AAO05308	AAO05308 Human pol
38	38	61.5	121	4	AAO05517	AAO05517 Human pol
39	39	60.3	31	2	AAW12916	AAW12916 Octopepti
40	40	59.0	128	4	AAO04686	AAO04686 Human pol
41	46	59.0	996	9	ADX39977	ADX39977 HIV pol p
42	46	59.0	1002	9	ADX39946	ADX39946 HIV pol p
43	46	59.0	1003	9	ADX39988	ADX39988 HIV pol p
44	46	59.0	1011	9	ADX39928	ADX39928 HIV pol p
45	46	59.0	1011	9	ADX40087	ADX40087 HIV pol p
46	46	59.0	1014	2	AAW68474	AAW68474 HIV-1 str
47	46	57.7	194	6	ABU23111	ABU23111 Protein e
48	45	57.7	317	2	AAW73507	AAW73507 Human ATG
49	45	57.7	317	6	AAW37816	AAW37816 Human sec
50	45	57.7	317	6	ADA38289	ADA38289 Human sec
51	45	57.7	317	8	ADM67242	ADM67242 Human hom
52	45	57.7	317	8	ADP56062	ADP56062 Human PRO
53	45	57.7	1018	3	AAO01769	AAO01769 Staphy
54	44	56.4	122	4	AAO02187	AAO02187 Candida a
55	44	56.4	587	5	ABP73497	ABP73497 Candida a
56	44	55.1	111	4	AAO02430	AAO02430 Human pol
57	43	55.1	121	3	AAO01889	AAO01889 Arabidops
58	43	55.1	137	4	AAO03896	AAO03896 Human pol
59	43	55.1	143	3	AAO14888	AAO14888 Arabidops
60	43	55.1	144	8	ADR94816	ADR94816 Novel S.
61	43	55.1	144	9	AEA58686	AEA58686 Streptoco
62	43	55.1	1002	9	ADX40058	ADX40058 HIV pol p
63	43	55.1	1278	3	ABR18277	ABR18277 Plasmodu
64	42.5	54.5	106	3	AAO01991	AAO01991 Human sec
65	42	53.8	88	4	AAO03273	AAO03273 Human pol
66	42	53.8	137	4	AAO02310	AAO02310 Human pol
67	42	53.8	190	3	AAO25277	AAO25277 Arabidops
68	42	53.8	195	3	AAO33061	AAO33061 Arabidops
69	42	53.8	226	7	ADR31137	ADR31137 Human dia
70	42	53.8	250	5	ABG99159	ABG99159 Human end
71	42	53.8	272	3	AAO49440	AAO49440 Arabidops
72	42	53.8	274	3	AAO06974	AAO06974 Arabidops
73	42	53.8	292	4	ABR57977	ABR57977 Drosophi
74	42	53.8	295	3	AAO49439	AAO49439 Arabidops
75	42	53.8	297	3	AAO06973	AAO06973 Arabidops
76	42	53.8	314	6	ADA38292	ADA38292 Mouse sec
77	42	53.8	314	6	ADM67241	ADM67241 Murine ad
78	42	53.8	367	6	ADA83987	ADA83987 Human CDK
79	42	53.8	369	4	AAW79489	AAW79489 Human pro
80	42	53.8	369	4	AAW41589	AAW41589 Human pol
81	42	53.8	369	4	AAW41588	AAW41588 Human pol
82	42	53.8	424	4	ABR64443	ABR64443 Drosophi
83	42	53.8	455	7	ADC31549	ADC31549 Human nov
84	42	53.8	476	4	AAW78505	AAW78505 Human pro
85	42	53.8	500	4	AAW93943	AAW93943 Human pol
86	42	53.8	500	5	ABG95660	ABG95660 Human nuc
87	42	53.8	500	8	ADH44816	ADH44816 Human KRZ
88	42	53.8	500	8	ADL32095	ADL32095 Human pro
89	42	53.8	734	8	ADN22640	ADN22640 Bacteri
90	42	53.8	806	8	ADN22639	ADN22639 Bacteri
91	42	53.8	846	4	AAW39803	AAW39803 Human pol
92	42	53.8	861	7	ABR88619	ABR88619 Rice abio
93	42	53.8	881	5	ABR92593	ABR92593 Rice abio
94	42	53.8	897	5	ABR88650	ABR88650 Rice abio
95	42	53.8	920	7	AAW90383	AAW90383 Rice abio
96	42	53.8	955	4	AAW39802	AAW39802 Human pol
97	42	53.8	1146	8	ADP99073	ADP99073 C. albica

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OM nucleic - nucleic search, using sw model

Run on: May 7, 2006, 14:06:06 ; Search time 1173 Seconds  
(without alignments)  
9033.880 Million cell updates/sec

Title: US-10-666-851-1

Sequence: 1 gacgtgctgggagctgcgc.....gaagtagctctcaaaaaa 2602

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapect 1.0

Searched: 9306428 seqs, 2036268586 residues

Total number of hits satisfying chosen parameters: 18612856

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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19: /SIDSS/ptodata/1/pubpna/US60\_NEW\_PUB.seq:1.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2465.4	94.8	4469	US-11-245-147-203	Sequence 203, App
2	2465.4	94.8	4608	US-10-821-234-137	Sequence 137, App
3	417.4	16.0	475	US-11-004-762-19	Sequence 19, App1
4	370.4	14.2	630	US-10-301-480-560598	Sequence 560598,
5	370.4	14.2	630	US-10-301-480-1174007	Sequence 1174007,
6	231.4	8.9	926	US-11-245-147-5	Sequence 5, App1
7	228	8.8	1382	US-11-245-147-197	Sequence 197, App
8	226.4	8.7	1196	US-10-216-161A-414	Sequence 414, App
9	176.6	6.8	1745	US-11-051-720-28	Sequence 28, App1
10	164.8	6.3	882	US-11-245-147-80	Sequence 80, App1
11	116.6	4.5	2379	US-09-925-065A-678403	Sequence 678403,
12	114	4.4	4350	US-11-245-147-124	Sequence 124, App
13	114	4.4	4350	US-11-245-147-125	Sequence 125, App
14	114	4.4	4350	US-11-245-147-205	Sequence 205, App

15	105	4.0	1944	US-11-245-147-49	Sequence 49, App1
16	103	4.0	631	US-09-925-065A-68204	Sequence 68204, A
17	103	4.0	631	US-10-301-480-169443	Sequence 169443,
18	103	4.0	631	US-10-301-480-782852	Sequence 782852,
19	101.2	3.9	1983	US-11-245-147-206	Sequence 206, App
20	97.4	3.7	4770	US-11-136-527-299	Sequence 299, App
21	97.2	3.7	1935	US-11-136-527-186	Sequence 186, App
22	87.8	3.4	2811	US-11-067-231-154	Sequence 154, App
23	87.8	3.4	2814	US-11-054-281-21	Sequence 21, App1
24	83.2	3.2	2184	US-11-054-281-35	Sequence 35, App1
25	77.2	3.0	2561	US-11-127-877-26	Sequence 26, App1
26	75.6	2.9	2820	US-11-186-284-188	Sequence 188, App
27	75.6	2.9	2820	US-11-245-147-204	Sequence 204, App
28	75.6	2.9	2840	US-11-054-281-23	Sequence 23, App1
29	73	2.8	1898	US-11-136-527-2690	Sequence 2690, Ap
30	73	2.8	7391	US-10-511-937-629	Sequence 629, App
31	73	2.8	7391	US-11-152-366-17	Sequence 17, App1
32	73	2.8	7392	US-11-169-041-5	Sequence 5, App1
33	73	2.8	7392	US-11-245-147-177	Sequence 177, App
34	73	2.8	7392	US-11-245-147-208	Sequence 208, App
35	61	2.3	2607	US-11-136-527-630	Sequence 630, App
36	61	2.3	14055	US-10-496-351-1	Sequence 1, App1
37	61	2.3	82746	US-10-496-351-56	Sequence 56, App1
38	59	2.3	1484	US-11-184-005-3	Sequence 3, App1
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41	55.8	2.1	1011	US-10-496-351-46	Sequence 46, App1
42	55.8	2.1	11905	US-10-496-351-57	Sequence 57, App1
43	53.6	2.1	604	US-11-136-527-1354	Sequence 1354, Ap
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45	52.2	2.0	600	US-11-136-527-5450	Sequence 5450, Ap

## ALIGNMENTS

RESULT 1  
US-11-245-147-203  
; Sequence 203, Application US/11245147  
; Publication No. US20060030541A1  
; GENERAL INFORMATION:  
; APPLICANT: GARCIA, TERESA  
; APPLICANT: ROMAN ROMAN, SERGIO  
; APPLICANT: BARON, ROLAND  
; APPLICANT: CALL, KATHERINE  
; APPLICANT: THREILHAR, JOACHIM  
; APPLICANT: CONNOLLY, TIMOTHY  
; APPLICANT: JACKSON, AMANDA  
; APPLICANT: BUSHNELL, STEVEN  
; APPLICANT: RANADI, GEORGES  
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE  
; FILE REFERENCE: 37991-0023  
; CURRENT APPLICATION NUMBER: US/11/245,147  
; CURRENT FILING DATE: 2005-10-07  
; PRIOR APPLICATION NUMBER: PCT/IB02/02211  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 60/281,400  
; PRIOR FILING DATE: 2001-04-05  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 203  
; LENGTH: 4469  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Homo sapiens secreted fibrinized-related protein 1  
; OTHER INFORMATION: (SFRP), mRNA.  
US-11-245-147-203

Query Match 94.8%; Score 2465.4; DB 18; Length 4469;  
Best Local Similarity 98.3%; Pred. No. 0;  
Matches 2553; Conservative 16; Indels 28; Gaps 5;





GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 7, 2006, 13:44:04 ; Search time 9249 Seconds  
(without alignments)  
13162.503 Million cell updates/sec

Title: US-10-666-851-1  
Perfect score: 2602  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	794.4	30.5	1011	5 BU196604	AGENCOURT
4	762	29.3	837	1 AU131621	AGENCOURT
5	758.2	29.1	763	8 CX786676	HRS3C 63
6	757.8	29.0	2298	4 AK081052	Mus muscu
7	755.2	29.0	762	7 CN271890	170004245
8	744.8	28.6	946	6 BC004466	Homo sapi
9	732	28.1	814	6 CD644680	AGENCOURT
10	731.2	28.1	913	5 BO879583	AGENCOURT
11	723	27.8	803	6 CD616079	56076764J
12	708.6	27.2	922	5 BO932355	AGENCOURT
13	679.4	26.1	823	1 AU127052	AU127052
14	676.2	26.0	801	8 CX781693	HRS3C 8 B
15	669.6	25.7	779	6 CN271889	170006001
16	668	25.7	722	7 CN247875	UI-M-F10-
17	660.2	25.4	741	6 CR769220	DKFZ469B
18	658.6	25.3	738	5 BO771388	UI-M-F10-
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21	637.2	24.5	756	6 CD616078	56076764H
22	633.2	24.3	907	2 BG119546	602347246

C	23	633	24.3	655	3	BI481260
	24	624	24.0	874	3	BP383443
	25	618.2	23.6	1003	5	BQ955732
	26	614.2	23.3	631	7	CN271885
	27	608.2	23.4	613	6	CB149331
	28	606.4	23.3	911	2	BG120989
	29	602.2	23.1	713	6	CB525580
	30	600.8	23.1	604	7	CN271888
	31	600.8	23.1	685	6	CF727313
	32	597.6	23.0	606	5	BX483569
	33	591.6	22.7	662	2	BB647191
	34	589.6	22.7	748	6	CB247054
	35	577.2	22.2	582	3	BP269186
	36	576.6	22.2	597	3	BP268522
	37	576.2	22.1	724	6	CB956696
	38	575.6	22.1	779	6	CD643855
	39	573.8	22.1	929	2	BG118192
	40	569.4	21.9	580	3	BP268745
	41	566.2	21.8	571	2	BP057567
	42	564.2	21.7	580	3	BP266267
	43	563.2	21.6	580	3	BP266621
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#### ALIGNMENTS

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LOCUS  
DEFINITION  
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fizzled-related sequence protein 1, full insert sequence.

ACCESSION  
AK088868  
VERSION  
AK088868.1 GI:26104967  
KEYWORDS  
HTC; CAP trapper.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1 Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
10349636

REFERENCE  
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
11042159

REFERENCE  
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Kono, H., Akiyama, T., Nishi, K., Kikunaga, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Kashiwagi, K.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Togawa, Y., Ozawa, K., Tanaka, T., Matsuzaki, S.,  
Yoneda, Y., Ishikawa, T., Obara, E., Watabiki, M.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
11076861

REFERENCE  
4 The RIKEN Genome Exploration Research Group Phase II Team and the  
PANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
5 The PANTOM Consortium and the RIKEN Genome Exploration Research

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OM nucleic - nucleic search, using sw model

Run on: May 7, 2006, 13:55:19 ; Search time 1855 Seconds  
(without alignments)  
11599.419 Million cell updates/sec

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Scoring table: IDENTITY NUC  
Gapop 10'-0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
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#### SUMMARIES

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13	2465.4	96.8	4469	9	US-10-756-149-3306
14	1803.8	69.3	2078	6	US-10-138-434A-1
15	1787.8	68.7	2075	6	US-10-138-434A-2
16	1787.8	68.7	2075	6	US-10-425-586-1
17	1787.8	68.7	2075	7	US-10-466-136-1
18	1483.4	57.0	3215	3	US-09-925-301-51
19	1076.2	41.4	1308	7	US-10-146-474-18
20	1076.2	41.4	1308	7	US-10-301-764-18
21	912.6	35.1	942	6	US-10-425-586-2
22	912.6	35.1	942	6	US-10-466-136-2
23	909.6	35.0	1017	6	US-10-425-586-9

24	697	26.8	804	6	US-10-425-586-12	Sequence 12, Appl
25	634	24.4	741	6	US-10-425-586-11	Sequence 11, Appl
26	603.2	23.2	2124	6	US-10-138-434A-26	Sequence 26, Appl
C 27	485.2	18.6	501	3	US-09-954-531-885	Sequence 885, Appl
C 28	485.2	18.6	501	3	US-09-954-531-1298	Sequence 1298, Appl
C 29	485.2	18.6	501	9	US-10-843-641A-1952	Sequence 1952, Appl
C 30	485.2	18.6	501	9	US-10-843-641A-2365	Sequence 2365, Appl
31	481.6	18.5	588	6	US-10-425-586-10	Sequence 10, Appl
32	444	17.1	690	6	US-10-425-586-13	Sequence 13, Appl
33	427.6	16.4	445	7	US-10-242-535A-43352	Sequence 43352, A
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35	401.2	15.4	1905	6	US-10-338-604-1	Sequence 1, Appl1
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#### ALIGNMENTS

RESULT 1  
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; Publication No. US20040115195A1  
; GENERAL INFORMATION:  
; APPLICANT: Bodine, Peter  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS USING SECRETED FRIZZLED  
; FILE REFERENCE: 00630/1000091-US1  
; CURRENT APPLICATION NUMBER: US/10/666,851  
; CURRENT FILING DATE: 2003-09-19  
; PRIOR APPLICATION NUMBER: US 10/169,545  
; PRIOR FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: US 60/412,379  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2602  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-666-851-1

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Matches 2602; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 GATTCGCTGGGAGCTGGCGCTTTGTCCCGGAGGCTTGGAGTTGGCGGAGCGC 60  
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GenCore version 5.1.8  
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(without alignment)

11428.424 Million cell updates/sec

Title: US-10-666-851-1

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Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

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Post-processing: Minimum Match 0%

Maximum Match 100%  
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9: gb\_ro:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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13	1844.6	70.9	2094	8	AF017987 Homo sapi
14	1803.8	69.3	2078	8	AR253205 Sequence
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16	1802.8	69.3	188270	8	AC104393 Homo sapi
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21	1787.8	68.7	2075	6	AX565707 Sequence
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ACCESSION	AX099741.1	GI:13538784			
VERSION	AX099741.1				
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SOURCE					
ORGANISM	Homo sapiens (human)				
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo.				
REFERENCE					
AUTHORS	Bodine, P.V.				
TITLE	Pharmaceutical compositions and methods of using secreted fibrinized related protein				
JOURNAL	Patent: WO 0119855-A 1 22-MAR-2001;				
	American Home Products Corporation (US)				
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